INPUT SET: S30271.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                        SEQUENCE LISTING        ENTERED
 2
 3   (1)   General Information:
 4
 5        (i)  APPLICANT: KAYAGAKI, Nobuhiko
 6                       YAGITA, Kideo
 7                       OKUMURA, Ko
 8                       NAKATA, Motomi
 9
10       (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
11               REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
12
13      (iii) NUMBER OF SEQUENCES: 31
14
15       (iv) CORRESPONDENCE ADDRESS:
16            (A) ADDRESSEE: McDermott, Will & Emery
17            (B) STREET: 99 Canal Center Plaza, Suite 300
18            (C) CITY: Alexandria
19            (D) STATE: Virginia
20            (E) COUNTRY: USA
21            (F) ZIP: 22314
22
23        (v) COMPUTER READABLE FORM:
24            (A) MEDIUM TYPE: Floppy disk
25            (B) COMPUTER: IBM PC compatible
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29       (vi) CURRENT APPLICATION DATA:
30            (A) APPLICATION NUMBER: US 08/913,555
31            (B) FILING DATE: 19-SEP-1997
32            (C) CLASSIFICATION:
33
34     (viii) ATTORNEY/AGENT INFORMATION:
35            (A) NAME: Bucca Ph.D., Daniel
36            (B) REGISTRATION NUMBER: 42,368
37            (C) REFERENCE/DOCKET NUMBER: 50356-150
38
39       (ix) TELECOMMUNICATION INFORMATION:
40            (A) TELEPHONE: 202-756-8600
41            (B) TELEFAX: 202-756-8699
42
43
44   (2) INFORMATION FOR SEQ ID NO:1:
45
46        (i) SEQUENCE CHARACTERISTICS:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/913,555*

INPUT SET: S30271.raw

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47              (A) LENGTH: 120 amino acids
48              (B) TYPE: amino acid
49              (C) STRANDEDNESS: single
50              (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: peptide
53
54
55
56
57      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59      Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
60      1               5                   10              15
61
62      Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp
63                  20                  25                  30
64
65      Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly
66          35                  40                  45
67
68      Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys
69          50                  55                  60
70
71      Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
72      65                  70                  75                  80
73
74      Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
75                      85                  90                  95
76
77      Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln
78                  100                 105                 110
79
80      Gly Thr Thr Val Thr Val Ser Ser
81              115                 120
82
83  (2) INFORMATION FOR SEQ ID NO:2:
84
85      (i) SEQUENCE CHARACTERISTICS:
86              (A) LENGTH: 360 base pairs
87              (B) TYPE: nucleic acid
88              (C) STRANDEDNESS: double
89              (D) TOPOLOGY: linear
90
91      (ii) MOLECULE TYPE: cDNA to mRNA
92
93
94
95
96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
97
98  GTGCAGCTGC AGGAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATTTCC        60
99
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100   TGCAAGGCTT CTGGCTATGC ATTCAGTAGC TCCTGGATGA ACTGGGTGAA GCAGAGGCCT      120
101
102   GGAAAGGGTC TTGAGTGGAT TGGACGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC      180
103
104   GGGAAGTTCA AGGGCAAGGC CACACTGACC GCAGACAAAT CCTCCAGCAC AGCCTACATG      240
105
106   CAACTCAGCA GTCTGACATC TGAGGACTCT GCGGTCTACT TCTGTGCAAG ATCGTATTAC      300
107
108   TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA      360
109
110
111   (2) INFORMATION FOR SEQ ID NO:3:
112
113       (i) SEQUENCE CHARACTERISTICS:
114           (A) LENGTH: 108 amino acids
115           (B) TYPE: amino acid
116           (C) STRANDEDNESS: single
117           (D) TOPOLOGY: linear
118
119      (ii) MOLECULE TYPE: peptide
120
121
122
123
124      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
125
126       Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
127       1               5                   10                  15
128
129       Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
130                   20                  25                  30
131
132       Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
133               35                  40                  45
134
135       Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
136           50                  55                  60
137
138       Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
139       65                  70                  75                  80
140
141       Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
142                   85                  90                  95
143
144       Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
145                   100                 105
146
147   (2) INFORMATION FOR SEQ ID NO:4:
148
149       (i) SEQUENCE CHARACTERISTICS:
150           (A) LENGTH: 324 base pairs
151           (B) TYPE: nucleic acid
152           (C) STRANDEDNESS: double
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153              (D) TOPOLOGY: linear
154
155        (ii) MOLECULE TYPE: cDNA to mRNA
156
157
158
159
160        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
161
162   GACATCCAGA TGACGCAGTC TCCATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC      60
163
164   ATCAGTTGCA GGGCAAGTCA GGATATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA     120
165
166   GATGGAACTG TTAAACTCCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA     180
167
168   AGGTTCAGTG GCAGTGGGTC TGGGACAGAT TATTCTCTCA CCATCAGCAA CCTGGAACCT     240
169
170   GAAGATATTG CCACTTACTT TTGTCAGCAA TATAGTGAAT TTCCGTGGAC GTTCGGTGGA     300
171
172   GGCACCAAGC TGGAAATCAA ACGG                                            324
173
174   (2) INFORMATION FOR SEQ ID NO:5:
175
176        (i) SEQUENCE CHARACTERISTICS:
177              (A) LENGTH: 118 amino acids
178              (B) TYPE: amino acid
179              (C) STRANDEDNESS: single
180              (D) TOPOLOGY: linear
181
182        (ii) MOLECULE TYPE: peptide
183
184
185
186
187        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
188
189        Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser
190        1               5                   10                  15
191
192        Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr Trp
193                    20                  25                  30
194
195        Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
196                    35                  40                  45
197
198        Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
199             50                  55                  60
200
201        Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met
202        65                  70                  75                  80
203
204        Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
205.                     85                  90                  95
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/913,555*

DATE: 12/10/98
TIME: 12:58:39

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206
207        Arg Tyr Arg Asp Tyr Asp Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
208                    100                 105                 110
209
210        Thr Val Thr Val Ser Ser
211                115
212
213    (2) INFORMATION FOR SEQ ID NO:6:
214
215        (i) SEQUENCE CHARACTERISTICS:
216             (A) LENGTH: 354 base pairs
217             (B) TYPE: nucleic acid
218             (C) STRANDEDNESS: double
219             (D) TOPOLOGY: linear
220
221    (ii) MOLECULE TYPE: cDNA to mRNA
222
223
224
225
226        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
227
228    GTGCAGCTGC AGCAGTCAGG AGCTGAGCTG GTAAGGCCTG GGACTTCAGT GAAGATGTCC      60
229
230    TGCAAGGCTG CTGGATACAC CTTCACTAAC TACTGGATAG GTTGGGTAAA GCAGAGGCCT     120
231
232    GGACATGGCC TTGAGTGGAT TGGATATCTT TACCCTGGAG GTCTTTATAC TAACTACAAT     180
233
234    GAGAAGTTCA AGGGCAAGGC CACACTGACT GCAGACACAT CCTCCAGCAC AGCCTACATG     240
235
236    CAGCTCAGCA GCCTGACATC TGAGGACTCT GCCATCTATT ACTGTGCAAG ATACAGGGAT     300
237
238    TACGACTATG CTATGGACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA           354
239
240    (2) INFORMATION FOR SEQ ID NO:7:
241
242        (i) SEQUENCE CHARACTERISTICS:
243             (A) LENGTH: 113 amino acids
244             (B) TYPE: amino acid
245             (C) STRANDEDNESS: single
246             (D) TOPOLOGY: linear
247
248    (ii) MOLECULE TYPE: peptide
249
250
251
252
253        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
254
255        Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly
256         1                 5                 10                  15
257
258        Asp Gln Ala Ser Ile S r Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/913,555*

INPUT SET: S30271.raw

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